

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17 ; Search time: 21:357; Seconds  
(without alignments)  
58 517 Million cell updates/sec

Title: US-09-856-070-19

Perfect score: 65

Sequence: 1 KEPMMLQWVF 13

Scoring table: BLASTW62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 65    | 100.0         | 581    | 2     | 145889      |
| 2          | 65    | 100.0         | 586    | 1     | A34400      |
| 3          | 65    | 100.0         | 630    | 2     | T47177      |
| 4          | 62    | 95.4          | 586    | 1     | B41129      |
| 5          | 41    | 63.1          | 327    | 2     | T42999      |
| 6          | 41    | 63.1          | 365    | 2     | T37720      |
| 7          | 40    | 61.5          | 218    | 2     | S75100      |
| 8          | 40    | 61.5          | 577    | 1     | A41390      |
| 9          | 40    | 61.5          | 577    | 1     | S39804      |
| 10         | 40    | 61.5          | 583    | 1     | A46127      |
| 11         | 40    | 61.5          | 583    | 1     | S39805      |
| 12         | 40    | 61.5          | 583    | 1     | A41129      |
| 13         | 40    | 61.5          | 1263   | 2     | T15496      |
| 14         | 39    | 60.0          | 250    | 2     | B84312      |
| 15         | 39    | 60.0          | 405    | 2     | B36340      |
| 16         | 39    | 60.0          | 413    | 2     | A31951      |
| 17         | 39    | 60.0          | 414    | 2     | C90364      |
| 18         | 39    | 60.0          | 584    | 2     | S75944      |
| 19         | 39    | 60.0          | 890    | 2     | T75103      |
| 20         | 38    | 58.5          | 85     | 2     | E96544      |
| 21         | 38    | 58.5          | 130    | 2     | B84333      |
| 22         | 38    | 58.5          | 132    | 2     | E90833      |
| 23         | 38    | 58.5          | 132    | 2     | E90900      |
| 24         | 38    | 58.5          | 145    | 2     | E95690      |
| 25         | 38    | 58.5          | 150    | 2     | A97449      |
| 26         | 38    | 58.5          | 150    | 2     | A92667      |
| 27         | 38    | 58.5          | 467    | 1     | A49377      |
| 28         | 38    | 58.5          | 533    | 2     | T27499      |
| 29         | 38    | 58.5          | 756    | 2     | T00367      |

apolipoprotein B -  
hypothetical prote  
M protein precursor  
M protein type 18  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
cheA activity-modu  
2,3 dihydroxybiphe  
protein-export mem  
conserved hypothet  
fodrin alpha chain  
hypothetical prote  
hypothetical prote

## ALIGNMENTS

### RESULT 1

145889

carin - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15 Oct 1996 #sequence\_revision 15 Oct 1996 #text\_change 13-Aug-1999

C:Accession: 145889

R:Berqson, C M; Zhao, H; Saijoh, K; Duman, P S; Nestler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A>Title: Ezrin and osteocalcin, two proteins associated with cell shape and growth, a

A:Reference number: 145889

A:Accession: 145889

A>Status: preliminary: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-581 <REP>

A:Cross-references: M09439, N01936319, P11N AAA30510, L101329408

C:Subfamily: ezrin, protein 4.1 membrane binding domain homolog

E7-291/Domain, protein 4.1 membrane-binding domain homology 3411-

Query Match 100.0%; Score 65; DB 2; Length 581;

Best Local Similarity 100.0%; Pred No 0.0027;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13

DB 344 KEELMLRLQDYEE 356

### RESULT 2

A34400

ezrin [validated] - human

S:Alternate names: cyto villin, p81 protein, villin 2

C:Species: Homo sapiens (man)

C>Date: 22-Jun-1999 #sequence\_revision 14-Jul-1991 #text\_change 08 Dec 2000

C:Accession: A34400; S092633; P61092

R:Toranaga, O.; Wajsbust, R.; Pakkath, B.; Grzeschik, K.H.; Wallstroom, L.; Valeri, A.

J. Biol. Chem. 264, 16727-16732, 1989

A>Title: Cyto villin, a microvillar M-r 75,000 protein-cDNA sequence, prokaryotic exp

A:Reference number: A34400; M01D-R4380299; PMID:2674140

A:Accession: A34400

A:Molecule type: mRNA

A:Residues: 1-586 <REP>

A:Cross-references: GB:05021

A>Note: The translation of residues 1-11 is not given

A>Note: parts of this sequence were confirmed by protein sequencing

R:Gould, K.H.; Brutscher, A.; Esch, F.S.; Hunter, T.

EMBO J. 8, 4133-4142, 1989

A>Title: cDNA cloning and sequencing of the protein tyrosine kinase substrate, ezrin,

A:Reference number: S092633; M01D-R4380299; PMID:2591371

A:Accession: S092633

A:Molecule type: mRNA

A:Residues: 2-586 <REP>

A:Cross-references: GB:05021, N01936319, P11N AAA30510, L101329408

R:Baum, G.; Rasmussen, H.H.; Van den Bulecke, M.; Van Damme, J.; Fuyter, M.; Gesser, B.; G. Electrophoresis 11, 528-536, 1990  
 A:Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing  
 A:Reference number: A61002; PMID:91031404; PMID:1699755  
 A:Accession: E61002

A:Molecule type: protein  
 A:Residues: 255-253;194;197;196-199;197;201;204 270 <BAU>  
 A:Note: It is not certain whether this material represents ezrin or radixin (see entry A61002). This material corresponds to transformed epithelial anion cell (EMA) database  
 A:Comment: This protein is located in microvilli and is proposed to play a role in modulation of cell motility

A:Gene: GDB:V112  
 A:Cross references: GDB:120489; OMIM:129000  
 A:Map position: 6q25.6q26  
 A:Superfamily: ezrin, protein 4.1 membrane binding domain homology  
 A:Keywords: actin binding; cytoskeleton; membrane associated protein; phosphoprotein  
 F:2-586/Product: ezrin #status experimental <MAT>  
 F:7-291/Domain: protein 4.1 membrane binding domain homology <MAT>  
 F:553-586/Region: actin binding #status predicted  
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted  
 F:214-299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 586;  
 Best Local Similarity 100.0%; Pred. No. 0.0029;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13  
 |||||  
 Db 344 KEELMLRLQDYEE 356

## RESULT 4

T47177  
 hypothetical protein DKFZp762H157.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
 C:Accession: T47177

R:Kroonwelder, H.; Obermaier, B.; McWes, H.W.; Weil, H.; Wiemann, S.  
 submitted to the Protein Sequence Database, March 2000  
 A:Reference number: 22477  
 A:Accession: T47177

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-640 <AAA>  
 A:Cross references: EMBL:AL162086  
 A:Experimental source: adult melanoma (Mewo cell line); cl-onc DKFZp762H157  
 A:Genetics:  
 C:Superfamily: ezrin; protein 4.1 membrane binding domain homology

Query Match 100.0%; Score 65; DB 2; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13  
 |||||  
 Db 388 KEELMLRLQDYEE 400

## RESULT 4

M41129  
 ezrin - mouse  
 N:Alternate names: cyto villin; p81 protein; radixin; villin 2  
 C:Species: Mus musculus (house mouse)

C:Date: 03-Aug-1992 #sequence\_revision 14-Jul-1994 #text\_change 22-Jun-1999  
 C:Accession: M41129; E64501; A45501; S24200  
 R:Fujidama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.  
 J. Cell Biol. 115, 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.  
 A:Reference number: A41129; PMID:9264635; PMID:1955455  
 A:Accession: M41129  
 A:Molecule type: mRNA  
 A:Residues: 1-586 <FUN>

A:Cross references: EMBL:X60671; M495089; EMBL:CAAA4086.1; F01045088  
 R:Rigton, M.; Burgess, W.H.; Chen, D.; Draker, H.J.; Bretscher, A.; Samelson, L.E.  
 J. Immunol. 149, 1847-1852, 1992  
 A:Title: Identification of ezrin as an 81-kDa tyrosine phosphorylated protein in T cell  
 A:Reference number: A45501; MUID:92388649; PMID:1381389  
 A:Accession: C46501

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 412-426 <EGE>  
 A:Experimental source: MRL lpr/lpr, T-cells  
 A:Note: sequence extracted from NCBI backbone (NCBI:P112938)  
 A:Accession: A46501

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 47-33;E' <EG2>  
 A:Experimental source: MRL lpr/lpr, T-cells  
 A:Note: sequence extracted from NCBI backbone (NCBI:P112938)  
 A:Accession: M46501

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 53-57;158;159-159;152-155 <EG3>  
 A:Experimental source: MRL lpr/lpr, T-cells

A:Note: sequence extracted from NCBI backbone (NCBI:P112940)  
 C:Comment: This protein is located in microvilli and is proposed to play a role in microvilli  
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology  
 C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosphoprotein; actin binding; ezrin #status predicted <MAT>  
 F:7-291/Domain: protein 4.1 membrane-binding domain homology <MAT>  
 F:553-586/Region: actin binding #status predicted  
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted  
 F:214-299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 95.4%; Score 62; DB 1; Length 586;  
 Best Local Similarity 92.3%; Pred. No. 0.009;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13  
 |||||  
 Db 344 KEELMLRLQDYEE 356

## RESULT 5

T42999  
 ethanalamine phosphate cytidyl:transferrase homology fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42999

R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.  
 DNA Res. 4, 363-369, 1997  
 A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.  
 A:Reference number: 217323; MUID:98162722; PMID:9501991  
 A:Accession: T42999

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-327 <YOS>  
 A:Cross references: EMBL:D89199; MUID:q1749605; PIDN:HAAL3860.1; PID:q1749606  
 A:Experimental source: strain PR745

Query Match 63.1%; Score 41; DB 2; Length 327;  
 Best Local Similarity 61.5%; Pred. No. 19;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13  
 |||||  
 Db 295 KQVMLPQHYEE 307

## RESULT 6

T37720  
 ethanalamine phosphate cytidyl:transferrase (EC 2.7.7.14) - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T37720

R.Murphy, J. Harris, D. J. Barrett, R. G. Rajandream, M. A. Typas, M. H.  
 submitted to the EMBL Data Library, August 1999  
 A:Reference number: Z17349  
 A:Accession: T37720  
 A:Status: preliminary; translated from GE/EMBL/DDRI  
 A:Molecule type: DNA  
 A:Residues: 1365 <MOL>  
 A:Cross-references: EMBL:AL09770; PIDN:AA52424.1; EMBL:U000566; SDB:SPAC15E1.05C  
 A:Experimental source: strain 9709; cosmid c15F1  
 C:Genetics:  
 A:Gene: SPDR:SPAC15E1.05C  
 A:Map position: 1  
 A:Introns: 23/71  
 C:Keywords: nucleotidyltransferase

Query Match 63.1% Score 41; DB 2; Length 365;  
 Best Local Similarity 61.5% Pred. No. 21;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13

DB 333 KQVMLRLQDYEE 345

RESULT 7

ABC transport protein - *Synechocystis* sp (strain PCC 6803)

N:Alternate names: protein sl10240

C:Species: *Synechocystis* sp

A:Variety: PCC 6803

C:Date: 25 Apr 1997 #sequence\_revision 25 Apr 1997 #text\_change 02-Feb 2001

A:Accession: S75100

R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

G. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A:Reference number: S74322; MCL:37061207; PMID:846731

A:Accession: S75100

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1218 <KAN>

A:Cross-references: EMBL:U000566; PIDN:AA11962.1; EMBL:U000566

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: short chain ATP binding cassette proteins, ATP binding cassette head 4;

C:Keywords: ATP; nucleotide binding; P-loop

F:17-210/Domain: ATP-binding cassette homology <ABC>

F:34-41/Region: nucleotide binding motif A (P-loop)

Query Match 61.5% Score 40; DB 2; Length 218;

Best Local Similarity 72.7% Pred. No. 18;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KEELMLRLQDY 11

DB 169 KFFITVILQDY 179

RESULT 8

A41289

moesin - human

N:Alternate names: membrane organizing extension spike protein

C:Species: *Homo sapiens* (man)

C:Date: 30-Jun-1993 #sequence\_revision 14-Jul-1994 #text\_change 22-Jun-1999

A:Accession: A41289

R.Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.

Proc Natl Acad Sci U S A 88, 8297-8301, 1991

A:Title: Moesin: a member of the protein 4.1-talin-ezrin family of proteins.

A:Reference number: A41289; MUID:52039840; PMID:1524389

A:Accession: A41289

A:Molecule type: mRNA

A:Residues: 1-577 <LAN>

A:Cross-references: GH M64906; NID:g18426; PIDN:AAA36322.1; PMID:188626

C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma  
 C:Genetics:  
 A:Gene: GDB:MSN  
 A:Cross-references: GDB:136819; OMIM:309845  
 A:Map position: Xq11.2-Xq12  
 C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology  
 C:Keywords: actin binding; cytoskeleton; membrane protein  
 F:2-577/Product: moesin #status predicted <MAT>  
 F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:544-577/Region: actin binding #status predicted

Query Match 61.5% Score 40; DB 1; Length 577;

Best Local Similarity 69.2% Pred. No. 50;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13

DB 344 KEELMERLQIEE 356

RESULT 9

S39804

moesin - pig

N:Alternate names: membrane organizing extension spike protein

C:Species: *Sus scrofa domestica* (domestic pig)

C:Date: 19-May-1994 #sequence\_revision 14-Jul-1991 #text\_change 22-Jun-1999

A:Accession: S39804

R.Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.

Biochim Biophys Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification

A:Reference number: S39804; MCL:34032743; PMID:828231

A:Accession: S39804

A:Molecule type: mRNA

A:Residues: 1-577 <LAN>

A:Cross-references: EMBL:M86450; NID:g164581; PIDN:AA03864.1; PID:g164582

C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton; membrane protein

F:2-577/Product: moesin #status predicted <MAT>

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:544-577/Region: actin binding #status predicted

Query Match 61.5% Score 40; DB 1; Length 577;

Best Local Similarity 69.2% Pred. No. 50;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMLRLQDYEE 13

DB 344 KEELMERLQIEE 356

RESULT 10

A46127

radixin - human

C:Species: *Homo sapiens* (man)

C:Date: 31-Sep-1993 #sequence\_revision 14-Jul-1991 #text\_change 22-Jun-1999

A:Accession: A46127

R.Wilgenbus, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.

Genomics 16, 194-206, 1993

A:Title: Molecular cloning, cDNA sequence, and chromosomal assignment of the human ra

A:Reference number: A46127; MUID:93252378; PMID:8486357

A:Accession: A46127

A:Molecule type: mRNA

A:Residues: 1-583 <WIL>

A:Cross-references: GH:U02320; NID:g407465; PIDN:AAA36541.1; PID:g407466

A:Note: sequence extracted from NCBI backbone (NCIN:131481, NCIN:131482)

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it

C:Genetics:

A:Gene: GDB:RDX

A:Cross-references: GDB:136270; OMIM:179410

A:Map position: 11q23-11q23

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:470-477/Region: proline-rich  
 F:550-583/Region: actin binding \*status predicted

Query Match 61.5% Score 40; DB 1; Length 583;  
 Best Local Similarity 66.2% Pred No. 51;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLODYEE 13

||||| ||| ||

DB 444 KEELMERLODYEE 356

RESULT 11

S59805

Radixin - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 19-May-1994 #sequence\_revision: 14 Jul-1994 #text\_change 22-Jun-1999

C:Accession: S59805

R:Linkers: W T - Schwartz-Albiez, P - Fortmayer, H

Biochim. Biophys. Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of

A:Reference number: S59804; MUID:94092743; PMID:8268231

A:Accession: S59805

A:Molecule type: mRNA

A:Residues: 1-583 <LAN>

A:Cross-references: GR:866444; EMBL:M86391; NID:q164585; PIDD:AA802865.1; PID:q164586

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it is

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding \*status predicted

Query Match 61.5% Score 40; DB 1; Length 583;  
 Best Local Similarity 66.2% Pred No. 51;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLODYEE 13

||||| ||| ||

DB 444 KEELMERLODYEE 356

RESULT 12

A41129

Radixin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Aug-1992 #sequence\_revision: 14 Jul-1994 #text\_change 05-Sep-1997

C:Accession: A41129; S24201

R:Funayama, N.; Nagaiuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.

J. Cell Biol. 115, 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.

A:Reference number: A41129; MUID:92064635; PMID:1955455

A:Accession: A41129

A:Molecule type: mRNA

A:Residues: 1-583 <FUN>

A:Cross-references: EMBL:X60672; NID:q1034049; PID:q1334260

A:Note: part of this sequence was confirmed by protein sequencing

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it is

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding \*status predicted

Query Match 61.5% Score 40; DB 1; Length 583;  
 Best Local Similarity 66.2% Pred No. 51;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLODYEE 13

||||| ||| ||

DB 444 KEELMERLODYEE 356

RESULT 13

T15496

hypothetical protein C14F5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence\_revision: 26-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T15496

R:Minx, P.

submitted to the EMBL Data Library, June 1995

A:Description: the sequence of C. elegans cosmid C14F5.

A:Reference number: Z18361

A:Accession: T15496

A:Status: preliminary; translated from GB/EMBL/DD87

A:Molecule type: DNA

A:Residues: 1-1263 <MIN>

A:Cross-references: EMBL:U29082; NID:q861384; PIDD:q861384; PIDD:AAA68402.1; CDSF:014F

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:C14F5.3

A:Info: 21/3 34 2 74/22 85/22 88/2 92 3 22/24 130/2 141 5 150/24 112

Query Match 61.5% Score 40; DB 2; Length 1263;  
 Best Local Similarity 61.5% Pred No. 110402;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLODYEE 13

||||| ||| ||

DB 909 REFQHAKLODYEE 921

RESULT 14

H84212

hypothetical protein Vnq0546c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence\_revision: 02-Feb-2001 #text\_change 16-Feb-2001

C:Accession: H84212

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, R.D.; Lacky

; Leitthausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja

Jung, K.H.; Alam, M.; Proittas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbhardt, H.; Lowe, J.M.

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: H84212

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: GB:AE004437, NID:q10580146, PIDD:AA019068.1; GSPDB:GN00138

C:Genetics:

A:Superfamily: 3-isopropylmalate dehydratase leuB chain

Query Match 60.0% Score 39; DB 2; Length 250;  
 Best Local Similarity 66.7% Pred No. 31;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HELMLRLODYEE 13

||||| ||| ||

DB 226 FEVVSRIQDYEE 237

RESULT 15

B36340

alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 4 precursor [validated] - human

N:Alternate names: CD15; EIAM-1 ligand fucosyltransferase (ELECT); FCT1A; FUC-1IV; myo

C:Species: Homo sapiens (man)

C>Date: 20-Apr-2000 #sequence\_revision: 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: B36340; A36340; A40976; A41292

R:Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, R.; Lizard, R.; Newman, R.; Chi-Ross

Cell 63, 1349-1356, 1990

A:Title: EIAM-1: a gene that directs the expression of an EIAM-1 ligand.

A:Reference number: A36340; MUID:91084863; PMID:1702034

A:Accession: B36340

A:Molecule type: mRNA  
A:Residues: 1-405 <GCEL>  
A:Cross-references: GB:M58597, NID:q182070, PIDN:AAA63173.1, FID:q182071  
A:Accession: A36340  
A:Molecule type: mRNA  
A:Residues: 'MPRLWNAKPKSCAWEKFWAEAPGAPGANSSEKIGPGE' 'SIPKKGAVPFWASWFAHLALAAKPAKHLGGAGC  
A:Cross-references: GB:M58597, NID:q182070, PIDN:AAA63173.1, FID:q182071  
A:Note: the codon used as an initiator for this translation is not in a good context for  
K:Low, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larson, R.D.; Marks, P.M.; Macher, B.A.  
J. Biol. Chem. 266, 17467-17477, 1991  
A:Title: Molecular cloning of a human fucosyltransferase gene that determines expression  
A:Reference number: A40976; MUID:91373370; PMID:1716630  
A:Accession: A40976  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-86, 'p', 88-405 <LOW>  
A:Cross-references: GB:M58597, NID:q182070, PIDN:AAA63173.1, FID:q182071  
R:Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.  
J. Biol. Chem. 266, 21777-21783, 1991  
A:Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but doe  
A:Reference number: A41202; MUID:92342084; PMID:1718983  
A:Accession: A41202  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-240, 'D', 242-400 <KUM>  
A:Cross-references: GB:S65161; NID:q239005; PIDN:AB20349.1; FID:q239006  
C:Genetics:  
A:Gene: GDB:FUT4; CML5; FCT3A; FUC-TIV  
A:Cross-references: GDB:131563; OMIM:104230  
A:Map position: 11q21-11q21  
C:Superfamily: galactoside 3(4)-L-fucosyltransferase  
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase  
F:1-48/Domain: signal sequence #status predicted <Sig>  
F:49-405/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAI>  
F:91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.0%; Score 39; DB 2, Length 405,  
Best Local Similarity 66.7%; Pred. No. 52;  
Matches 8; Conservative 2; Mismatches 2; Indels 0, Gaps 0;

QY 2 EELMLRLQDYEE 13  
||: ||: |||  
Db 136 EEVDRLRLDYEE 147

Search completed: January 16, 2003, 10:57:50  
Job time : 22.3571 secs

